AMENDMENTS TO THE SPECIFICATION

Please replace the title with the following amended title:

T20/DP178 ~~AND T21/DP107~~ IS AN ACTIVATOR ~~ARE ACTIVATORS~~ OF HUMAN PHAGOCYTE FORMYL PEPTIDE RECEPTORS

Please replace the paragraph at 29:13-30 with the following amended paragraph:

By using this computational protocol, genome sequence data bases such as maintained by various organizations including: www.tigr.org/tdb; www.genetics.wisc.edu; www.stanford.edu/~ball; hiv-web.lanl.gov; www.ncbi.nlm.nih.gov; www.ebi.ac.uk; pasteur.fr/other/biology; and www.genome.wi.mit.edu, ~~http://www.tigr.org/tdb; http://www.genetics.wisc.edu; http://genome-www.stanford.edu/~ball; http://hiv-web.lanl.gov; http://wwwncbi.nlm.nih.gov; http://www.ebi.ac.uk; http://pasteur.fr/other/biology; and http://www-genome.wi.mit.edu~~, can be rapidly screened for specific protein active sites and for identification of the residues at those active sites which resemble a desired ligand. Several other groups have developed databases of short sequence patterns or motifs designed to identify a given function or activity of a protein. These databases, notably Prosite (expasy.hcuge.ch/sprot/prosite.html; Blocks (www.blocks.fhcrc.org); and Prints (www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html), ~~(http://expasy.hcuge.ch/sprot/prosite.html); Blocks (http://www.blocks.fhcrc.org); and Prints (http://www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html)~~, use short stretches of sequence information to identify sequence patterns that are specific for a given function; thus they avoid the problems arising from the necessity of matching entire sequences. In this manner, new ligands are rationally selected for further identification by FPR class characterization assays, as described above. Rounds or cycles of functional assays on the molecules and derivatives thereof and further FFF refinement and database searching allows an investigator to more narrowly define classes of ligands which produce desirable inflammatory responses.